

SEQUENCE LISTING

<110> Clausen, Henrik

<120> UDP-N-Acetylglucosamine:

Galactose-beta-1,3-N-Acetylgalactosamine-alpha-R /
N-Acetylglucosamine-beta-1,3-N-Acetylgalactosamine-alpha-R (GlcNAc to GalNAc)
beta-1,6-N-Acetylglucosaminyltransferase, C2/4

<130> P199801704 WO JNY

<140>

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<150> DK PA 1988 01605

<151> 1998-12-04

<160> 10

<170> PatentIn Ver. 2.1

<210> 1

<211> 2319

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (496)..(1809)

<223> cDNA sequence

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gagaagctac taaaggattg tgtcctcctc caccttcctt gtgctcgggc tccacctgtc 480

tcccattctg tgacg atg gtt caa tgg aag aga ctc tgc cag ctg cat tac 531
 Met Val Gln Trp Lys Arg Leu Cys Gln Leu His Tyr
 1 5 10

ttg tgg gct ctg ggc tgc tat atg ctg ctg gcc act gtg gct ctg aaa 579
 Leu Trp Ala Leu Gly Cys Tyr Met Leu Leu Ala Thr Val Ala Leu Lys
 15 20 25

ctt tct ttc agg ttg aag tgt gac tct gac cac ttg ggt ctg gag tcc 627
 Leu Ser Phe Arg Leu Lys Cys Asp Ser Asp His Leu Gly Leu Glu Ser
 30 35 40

agg gaa tct caa agc cag tac tgt agg aat atc ttg tat aat ttc ctg 675
 Arg Glu Ser Gln Ser Gln Tyr Cys Arg Asn Ile Leu Tyr Asn Phe Leu
 45 50 55 60

aaa ctt cca gca aag agg tct atc aac tgt tca ggg gtc acc cga ggg 723
 Lys Leu Pro Ala Lys Arg Ser Ile Asn Cys Ser Gly Val Thr Arg Gly
 65 70 75

gac caa gag gca gtg ctt cag gct att ctg aat aac ctg gag gtc aag 771
 Asp Gln Glu Ala Val Leu Gln Ala Ile Leu Asn Asn Leu Glu Val Lys
 80 85 90

aag aag cga gag cct ttc aca gac acc cac tac ctc tcc ctc acc aga 819
 Lys Lys Arg Glu Pro Phe Thr Asp Thr His Tyr Leu Ser Leu Thr Arg
 95 100 105

gac tgt gag cac ttc aag gct gaa agg aag ttc ata cag ttc cca ctg 867
 Asp Cys Glu His Phe Lys Ala Glu Arg Lys Phe Ile Gln Phe Pro Leu
 110 115 120

agc aaa gaa gag gtg gag ttc cct att gca tac tct atg gtg att cat 915
 Ser Lys Glu Glu Val Glu Phe Pro Ile Ala Tyr Ser Met Val Ile His
 125 130 135 140

gag aag att gaa aac ttt gaa agg cta ctg cga gct gtg tat gcc cct 963
 Glu Lys Ile Glu Asn Phe Glu Arg Leu Leu Arg Ala Val Tyr Ala Pro
 145 150 155

cag aac ata tac tgt gtc cat gtg gat gag aag tcc cca gaa act ttc 1011
 Gln Asn Ile Tyr Cys Val His Val Asp Glu Lys Ser Pro Glu Thr Phe
 160 165 170

aaa gag gcg gtc aaa gca att att tct tgc ttc cca aat gtc ttc ata 1059
 Lys Glu Ala Val Lys Ala Ile Ile Ser Cys Phe Pro Asn Val Phe Ile
 175 180 185

gcc agt aag ctg gtt cgg gtg gtt tat gcc tcc tgg tcc agg gtg caa 1107
 Ala Ser Lys Leu Val Arg Val Val Tyr Ala Ser Trp Ser Arg Val Gln
 190 195 200

gct gac ctc aac tgc atg gaa gac ttg ctc cag agc tca gtg ccg tgg 1155
 Ala Asp Leu Asn Cys Met Glu Asp Leu Leu Gln Ser Ser Val Pro Trp
 205 210 215 220

aaa tac ttc ctg aat aca tgt ggg acg gac ttt cct ata aag agc aat 1203
 Lys Tyr Phe Leu Asn Thr Cys Gly Thr Asp Phe Pro Ile Lys Ser Asn
 225 230 235

gca gag atg gtc cag gct ctc aag atg ttg aat ggg agg aat agc atg 1251
 Ala Glu Met Val Gln Ala Leu Lys Met Leu Asn Gly Arg Asn Ser Met
 240 245 250

gag tca gag gta cct cct aag cac aaa gaa acc cgc tgg aaa tat cac 1299
 Glu Ser Glu Val Pro Pro Lys His Lys Glu Thr Arg Trp Lys Tyr His
 255 260 265

ttt gag gta gtg aga gac aca tta cac cta acc aac aag aag aag gat 1347
 Phe Glu Val Val Arg Asp Thr Leu His Leu Thr Asn Lys Lys Lys Asp
 270 275 280

cct ccc cct tat aat tta act atg ttt aca ggg aat gcg tac att gtg 1395
 Pro Pro Pro Tyr Asn Leu Thr Met Phe Thr Gly Asn Ala Tyr Ile Val
 285 290 295 300

gct tcc cga gat ttc gtc caa cat gtt ttg aag aac cct aaa tcc caa 1443
 Ala Ser Arg Asp Phe Val Gln His Val Leu Lys Asn Pro Lys Ser Gln
 305 310 315

caa ctg att gaa tgg gta aaa gac act tat agc cca gat gaa cac ctc 1491
 Gln Leu Ile Glu Trp Val Lys Asp Thr Tyr Ser Pro Asp Glu His Leu
 320 325 330

tgg gcc acc ctt cag cgt gca cgg tgg atg cct ggc tct gtt ccc aac 1539
 Trp Ala Thr Leu Gln Arg Ala Arg Trp Met Pro Gly Ser Val Pro Asn
 335 340 345

cac ccc aag tac gac atc tca gac atg act tct att gcc agg ctg gtc 1587
 His Pro Lys Tyr Asp Ile Ser Asp Met Thr Ser Ile Ala Arg Leu Val
 350 355 360

aag tgg cag ggt cat gag gga gac atc gat aag ggt gct cct tat gct 1635
 Lys Trp Gln Gly His Glu Gly Asp Ile Asp Lys Gly Ala Pro Tyr Ala
 365 370 375 380

ccc tgc tct gga atc cac cag cgg gct atc tgc gtt tat ggg gct ggg 1683
 Pro Cys Ser Gly Ile His Gln Arg Ala Ile Cys Val Tyr Gly Ala Gly
 385 390 395

gac ttg aat tgg atg ctt caa aac cat cac ctg ttg gcc aac aag ttt 1731
 Asp Leu Asn Trp Met Leu Gln Asn His His Leu Leu Ala Asn Lys Phe
 400 405 410

gac cca aag gta gat gat aat gct ctt cag tgc tta gaa gaa tac cta 1779
 Asp Pro Lys Val Asp Asp Asn Ala Leu Gln Cys Leu Glu Glu Tyr Leu
 415 420 425

cgt tat aag gcc atc tat ggg act gaa ctt tgagacacac tatgagagcg 1829
 Arg Tyr Lys Ala Ile Tyr Gly Thr Glu Leu
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ttgctacctg tggggcaaga gcatgtacaa acatgctcag aacttgctgg gacagtgtgg 1889

gtgggagacc agggctttgc aattcgtggc atcctttagg ataagagggc tgctattaga 1949

ttgtgggtaa gtagatcttt tgccttgcaa attgctgcct ggggtgaatgc tgcttgttct 2009

ctcaccctta accctagtag ttctccact aactttctca ctaagtgaga atgagaactg 2069

ctgtgatagg gagagtgaag gagggatatg tggtagagca cttgatttca gttgaatgcc 2129

tgctggtagc ttttccattc tgtggagctg ccgttcctaa taattccagg tttggtagcg 2189

tggaggagaa ctttgatgga aagagaacct tcccttctgt actgttaact taaaaataaa 2249

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tctaaacaga 2319

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<212> PRT

<213> Homo sapiens

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Gly Cys Tyr Met Leu Leu Ala Thr Val Ala Leu Lys Leu Ser Phe Arg
 20 25 30

Leu Lys Cys Asp Ser Asp His Leu Gly Leu Glu Ser Arg Glu Ser Gln
 35 40 45
 Ser Gln Tyr Cys Arg Asn Ile Leu Tyr Asn Phe Leu Lys Leu Pro Ala
 50 55 60
 Lys Arg Ser Ile Asn Cys Ser Gly Val Thr Arg Gly Asp Gln Glu Ala
 65 70 75 80
 Val Leu Gln Ala Ile Leu Asn Asn Leu Glu Val Lys Lys Lys Arg Glu
 85 90 95
 Pro Phe Thr Asp Thr His Tyr Leu Ser Leu Thr Arg Asp Cys Glu His
 100 105 110
 Phe Lys Ala Glu Arg Lys Phe Ile Gln Phe Pro Leu Ser Lys Glu Glu
 115 120 125
 Val Glu Phe Pro Ile Ala Tyr Ser Met Val Ile His Glu Lys Ile Glu
 130 135 140
 Asn Phe Glu Arg Leu Leu Arg Ala Val Tyr Ala Pro Gln Asn Ile Tyr
 145 150 155 160
 Cys Val His Val Asp Glu Lys Ser Pro Glu Thr Phe Lys Glu Ala Val
 165 170 175
 Lys Ala Ile Ile Ser Cys Phe Pro Asn Val Phe Ile Ala Ser Lys Leu
 180 185 190
 Val Arg Val Val Tyr Ala Ser Trp Ser Arg Val Gln Ala Asp Leu Asn
 195 200 205
 Cys Met Glu Asp Leu Leu Gln Ser Ser Val Pro Trp Lys Tyr Phe Leu
 210 215 220
 Asn Thr Cys Gly Thr Asp Phe Pro Ile Lys Ser Asn Ala Glu Met Val
 225 230 235 240
 Gln Ala Leu Lys Met Leu Asn Gly Arg Asn Ser Met Glu Ser Glu Val
 245 250 255
 Pro Pro Lys His Lys Glu Thr Arg Trp Lys Tyr His Phe Glu Val Val
 260 265 270
 Arg Asp Thr Leu His Leu Thr Asn Lys Lys Lys Asp Pro Pro Pro Tyr
 275 280 285

Asn Leu Thr Met Phe Thr Gly Asn Ala Tyr Ile Val Ala Ser Arg Asp
 290 295 300

Phe Val Gln His Val Leu Lys Asn Pro Lys Ser Gln Gln Leu Ile Glu
 305 310 315 320

Trp Val Lys Asp Thr Tyr Ser Pro Asp Glu His Leu Trp Ala Thr Leu
 325 330 335

Gln Arg Ala Arg Trp Met Pro Gly Ser Val Pro Asn His Pro Lys Tyr
 340 345 350

Asp Ile Ser Asp Met Thr Ser Ile Ala Arg Leu Val Lys Trp Gln Gly
 355 360 365

His Glu Gly Asp Ile Asp Lys Gly Ala Pro Tyr Ala Pro Cys Ser Gly
 370 375 380

Ile His Gln Arg Ala Ile Cys Val Tyr Gly Ala Gly Asp Leu Asn Trp
 385 390 395 400

Met Leu Gln Asn His His Leu Leu Ala Asn Lys Phe Asp Pro Lys Val
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Asp Asp Asn Ala Leu Gln Cys Leu Glu Glu Tyr Leu Arg Tyr Lys Ala
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Ile Tyr Gly Thr Glu Leu
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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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<210> 4

<211> 21

<212> DNA

<213> Artificial Sequence

<223> Description of Artificial Sequence: Primer

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<213> Artificial Sequence

<223> Description of Artificial Sequence: Primer

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<213> Artificial Sequence

<223> Description of Artificial Sequence: Primer

gtgggaactg tatgaacttc c

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<213> Artificial Sequence

<223> Description of Artificial Sequence: Primer

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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<212> DNA

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<223> Description of Artificial Sequence: Primer

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<210> 10

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